



SEQUENCE LISTING

<110> Kato, Seishi
Sekine, Shingo
Kimura, Tomoko
Kobayashi, Midori

<120> HUMAN PROTEINS HAVING SECRETORY SIGNAL
SEQUENCES AND DNAs ENCODING THESE PROTEINS

<130> GIN-6704CPUS

<140> US 09/254,760

<141> 1999-04-16

<150> JP 8/243,060

<151> 1996-09-13

<150> PCT/JP97/03239

<151> 1997-09-12

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<212> PRT

<213> Homo sapiens

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35 40 45
Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His
50 55 60
Arg Ser Arg Met Pro Lys Arg Ser Gly Ala Val Thr Ser Asp Thr
65 70 75
Leu Tyr Arg Ser Arg Leu Arg Lys Gly Lys Leu Tyr His Leu Lys Ala
80 85 90 95
Pro Pro Ser Val Cys Gln Pro Arg Glu Glu Met Gly Ser Gly Val His
100 105 110
Gln Leu Phe Gly Asp Glu Leu Gly Trp Arg Val Leu Glu Pro Glu Leu
115 120 125
Thr Gln Ile Cys Leu Phe Leu Leu Ala Leu Val Leu Ala Thr Val Ala
130 135 140 145

1-13
1-14

[illegible]

421. 158

CONCLUSIONS

1. *Chlorophyll a* (Chl *a*)

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Glu	Tyr	Ile	Ser	Gly	Tyr	Gln	Arg	Ser	Gln	Ile	Ile	Trp	Ile	Gly	Leu
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His	Asp	Pro	Gln	Lys	Arg	Gln	Gln	Trp	Gln	Trp	Ile	Asp	Gly	Ala	Met
			100					105					110		
Tyr	Leu	Tyr	Arg	Ser	Trp	Ser	Gly	Lys	Ser	Met	Gly	Gly	Asn	Lys	His
		115					120					125			
Cys	Ala	Glu	Met	Ser	Ser	Asn	Asn	Asn	Phe	Leu	Thr	Trp	Ser	Ser	Asn
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Ile	Val	Ala	Gly	Ser	Asn	Gly	Trp	Tyr	Asn	Tyr	Arg	His	Gln	Ala	Asp
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65				70					75					80	
Pro	Thr	Pro	Gly	Ile	Val	Ile	Asn	Arg	Pro	Asn	Gly	Thr	Asp	Val	Tyr
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Gln	Gly	Val	Pro	Lys	Asp	Tyr	Thr	Gly	Glu	Asp	Val	Thr	Pro	Gln	Asn
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Protein Data Bank, Brookhaven National Laboratory, New York, NY 10997

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 Thr Pro Ser Pro Asp Val Pro Leu Thr Ile Met Lys Arg Lys Leu Met
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 325 330 335
 Arg His Leu Asp Tyr Glu Tyr Ala Leu Arg His Leu Tyr Val Leu Val
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 65 70 75 80
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 Pro Gln Gly Lys Ser Tyr Leu Tyr Phe Thr Gln Phe Lys Ala Glu Val
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 115 120 125
 Glu Arg Glu Ser Asp Val Pro Leu Lys Thr Glu Glu Phe Glu Val Thr
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 Arg Val Glu Asn Val Ala Ser Ser Ser Gly Pro Met Arg Trp Trp Gln
 85 90 95
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 130 135 140
 Val Tyr Gln Tyr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val
 145 150 155 160
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 180 185 190
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 Gln Glu Val Gly Glu Ile Thr Asn Leu Arg Val Asn Phe Thr Arg Leu
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 275 280 285
 Asn Tyr Gln Arg Cys Ala Pro Ile Tyr Asn Asn Arg Arg Thr Arg Leu
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Tyr Arg Tyr Val Arg Thr Ser Leu Phe Tyr Leu Arg Asn Ser Leu

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 595 600 605
 Leu Trp Ser Gly Pro Gly Leu Glu Asp Arg Gly Leu Ala Ser Arg Ile
 610 615 620
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 625 630 635 640
 Pro Ala Val Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala Ile Leu
 645 650 655
 Ser Leu Arg Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro Leu Glu
 660 665 670
 Glu Gly Thr Leu Ser Leu Pro Arg Asp Leu His Ser Leu Asp Arg Ser
 675 680 685
 Leu Asn Gly Leu Leu Thr Met Tyr Gln Asn Lys Arg His Gln Pro Leu
 690 695
 Tyr Leu Ser Ser Ala Arg Pro Ser Gly Ala His Asn Val Glu Ser Pro
 705 710 715 720
 Ala Tyr Glu Gln Ser Ala Gln Ala Ala Gln Gln Val Ser Asp Ser Ser
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 Arg Leu Leu Asp Gln Leu Arg Asp Ser Arg Arg Gln Ala Glu Arg Leu
 740 745 750
 Val Arg Gln Ala Gly Gly Gly Gly Gly Thr Gly Ser Pro Lys Leu Val

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
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 35 40 45
 Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys
 50 55 60
 Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu
 65 70 75 80
 Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu
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 Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu
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 Thr Thr Asp Lys His Leu Ser Pro Asp Gly Gln Tyr Val Pro Arg Ile
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 Met Phe Val Asp Pro Ser Leu Thr Val Arg Ala Asp Ile Thr Gly Arg
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The following information is provided for the purpose of identifying the source of the material and for the purpose of providing a record of the material's history. The information is provided in the form of a table.

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aagagggcag agtggcagtg gatgtaggg accatctatc tatcacatc ctgggtctggc 360
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<212> DNA

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cdna

cdna

cdna

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1. *Chlorophyll a* (Chl *a*)

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400, 19

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110 ttt tga gat aag ata tga tgg aga gtc att gaa att gaa att aca 442
Leu Phe Gly Asp Glu Leu Gly Trp Arg Val Leu Glu Pro Glu Leu Thr
115 120 125

130 att taa atg tat atg att gat att atc ata gat taa gag att tcc 449
His Ile Cys Leu Phe Leu Leu Ala Leu Val Leu Ala Trp Glu Ala Ser
135 140 145

150 cct caa tat cct acc cca ccc gct cct tgaaggccc agattctacc 537
Pro His Tyr Pro Thr Pro Pro Ala Pro
155

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115 120 125

130 att taa atg tat atg att gat att atc ata gat taa gag att tcc 449
His Ile Cys Leu Phe Leu Leu Ala Leu Val Leu Ala Trp Glu Ala Ser
135 140 145

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Pro His Tyr Pro Thr Pro Pro Ala Pro
155

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Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile Asp			
70	75	80	
ggc gac aag gac ggg ttt gtc act gta gaa gag ctc aaa gac tgg att	347		
Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys Asp Trp Ile			
85	90	95	
aaa ttt gaa gaa aag ggc tgg att tat gag gaa gta gag gaa gaa tgg	395		
Lys Phe Ala Gln Lys Arg Trp Ile Tyr Glu Asp Val Glu Arg Gln Trp			
100	105	110	
aag ggg gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa	443		
Lys Gly His Asp Leu Asn Glu Asp Gly Leu Val Ser Trp Glu Glu Tyr			
115	120	125	
aaa aat gcc acc tac ggc tac gtt tta gat gat cca gat cct gat gat	491		
Lys Asn Ala Thr Tyr Gly Tyr Val Leu Asp Asp Pro Asp Pro Asp Asp			
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Gly Phe Asn Tyr Lys Gln Met Met Val Arg Asp Glu Arg Arg Phe Lys			
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Met Ala Asp Lys Asp Gly Asp Leu Ile Ala Thr Lys Glu Glu Phe Thr			
165	170	175	
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Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val Val			
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cag gaa gaa atg gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa	683		
Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile Asp			
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Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe Arg			
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Arg Lys Asn Arg Arg Lys Lys Met Arg Lys Glu Glu Thr Lys Arg Lys			
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Thr Lys Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr			
260	265	270	

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 ile Val Asp Lys Tyr Asp Leu Phe Val Gly Ser Gln Ala Thr Asp Phe
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Met Ala Ser Arg Ser Met Arg Leu Leu
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cta ttg ctg agc tgc ctg gcc aaa aca gga gtc ctg ggt gat atc atc 221
Leu Leu Leu Ser Cys Leu Ala Lys Thr Gly Val Leu Glv Asp Ile Ile
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Tyr Gly Tyr Phe Arg Lys Leu Arg Asn Trp Ser Asp Ala Glu Leu Glu
45 50 55

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Cys Gln Ser Tyr Gly Asn Gly Ala His Leu Ala Ser Ile Leu Ser Leu
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Lys Glu Ala Ser Thr Ile Ala Glu Tyr Ile Ser Gly Tyr Gln Arg Ser
75 80 85

cag ccg ata tgg att gcc ctg cac gac cca cag aag agg cag cag tgg 461
Gln Pro Ile Trp Ile Gly Leu His Asp Pro Gln Lys Arg Gln Gln Trp
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Gln Trp Ile Asp Gly Ala Met Tyr Leu Tyr Arg Ser Trp Ser Gly Lys
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Ser Met Gly Gly Asn Lys His Cys Ala Glu Met Ser Ser Asn Asn Asn
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Ile Leu Thr Trp Ser Ser Asn Ala Tyr Asn Lys Arg Gln His Ile Leu
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Cys Lys Tyr Arg Pro
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<221> misc feature
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 Met
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gtt cct ata gat gat cct gaa gat gga ggc aag cac tgg gtg gtg atc 215
 Val Pro Ile Asp Asp Pro Glu Asp Gly Gly Lys His Trp Val Val Ile
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gtg gca ggt tca aat ggc tgg tat aat tat agg cac cag gca gac ggc 263
 Val Ala Gly Ser Asn Gly Trp Tyr Asn Tyr Arg His Gln Ala Asp Ala
 35 40 45

tgc cat gcc tac cag atc att cac cgc aat ggg att cct gac gaa cag 311
 Cys His Ala Tyr Gln Ile Ile His Arg Asn Gly Ile Pro Asp Glu Gln
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 Ile Val Val Met Met Tyr Asp Asp Ile Ala Tyr Ser Gln Arg Asn Ile
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att cca att att att att att att att att att att att att att att 407
 Thr Ile Arg Val Val Ile Asn Ala Ile Asn Gly Thr Arg Val Tyr Gln
 95 100 105 110 115 120 125 130 135 140

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 Gly Val Pro Lys Asp Tyr Thr Gly Gln Asp Val Thr Pro Gln Asn Ile
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Thr Asp His Gly Ser Thr Gly Ile Leu Val Phe Irs Asn Glu Asp Leu	
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His Val Lys Asp Leu Asn Glu Phe Ile His Tyr Met Tyr Lys His Lys	
165 170 175	
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Met Tyr Arg Lys Met Val Phe Tyr Ile Glu Ala Cys Glu Ser Gly Ser	
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Met Met Asn His Leu Pro Asp Asn Ile Asn Val Tyr Ala Thr Thr Ala	
195 200 205	
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Ala Asn Pro Arg Glu Ser Ser Tyr Ala Cys Tyr Tyr Asp Glu Lys Arg	
210 215 220 225	
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Ser Thr Tyr Leu Gly Asp Trp Tyr Ser Val Asn Trp Met Glu Asp Ser	
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gac gtg gaa gat ctg act aaa gag aac ctg cac aag cag tac cnc ctg	887
Asp Val Glu Asp Leu Thr Lys Glu Thr Leu His Lys Gln Tyr His Leu	
245 250 255	
gta aaa tcc cac acc aac acc agc cac gtc atg cag tat gga aac aaa	935
Val Lys Ser His Thr Asn Thr Ser His Val Met Gln Tyr Gly Asn Lys	
260 265 270	
aca atc tcc acc atg aaa gta atg cag ttt cag ggt atg aac gta aaa	983
Thr Ile Ser Thr Met Lys Val Met Gln Phe Gln Gly Met Lys Arg Lys	
275 280 285	
gcc agt tet ccc gtc ccc cta cct cca gtc aca cac ctt gac ctc acc	1031
Ala Ser Ser Pro Val Pro Leu Pro Pro Val Thr His Leu Asp Leu Thr	
290 295 300 305	
atg atg atg gta gta gta gta gta gta gta gta gta gta gta gta gta	1079
Met Met Met Val Val Val Val Val Val Val Val Val Val Val Val Val	
310 315 320 325	
atg atg gat ctg gag gag tat atg atg ctg aac atg atg atg atg atg	1127
Thr Asn Asp Leu Glu Glu Ser Arg Glu Leu Thr Glu Glu Ile Glu Arg	
330 335 340	
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His Leu Asp Tyr Glu Tyr Ala Leu Arg His Leu Tyr Val Ile Val Asn	
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372

375

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 Leu Trp Ala Ala Leu Leu Leu Gly Ala Val Ala Leu Arg Pro Ala Glu
 15 20 25 30

gcg gtg tcc gag ccc acg acc gtg ggc ttt gac gtg cgg ccc ggc ggc 146
 Ala Val Ser Glu Pro Thr Thr Val Ala Phe Asp Val Arg Pro Gly Gly
 35 40 45

gtc gtg cat tcc ttc tcc cat aac gtg ggc cgg ggt ggc aac tat acg 194
 Val Val His Ser Phe Ser His Asn Val Gly Pro Gly Asp Lys Tyr Thr
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tat atg ttc atg tgc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 242
 Tyr Met His Thr Tyr Ala Ser Val Arg Gly Thr Asn Ala Val Trp Val
 245 250 255

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 Met Ser His Gly His Ser Val Arg His Val His His Thr Tyr Thr Thr
 295 300 305

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 Trp Arg His Val Val Val Val Val Val Val Val Val Val Val Val Val
 345 350 355

att aat aaa aca gca gta gtt aat aat aat ggg aca ttt aaa att gaa 481
 Val Thr Lys Thr Ala Val Ala His Arg Pro Gly Ala Phe Lys Ala His
 141 150 155

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 Met Gly Val Lys Leu
 1 5

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gag ata ttt cgg atg ata atc ttt ctt act ttc cct gta gtt atg ttt 164
 Glu Ile Phe Arg Met Ile Ile Tyr Leu Thr Phe Pro Val Ala Met Phe
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tgg gtt tcc aat aag gac gag tgg ttt gag gac gat gtc ata aag cgc 212
 Trp Val Ser Asn Gln Ala Glu Tyr Phe Gln Asp Asp Val Ile Gln Arg
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att att att att att att att att att att att att att att att att 26
 Lys Arg Glu Leu Trp Ile Ile Arg Lys Leu Glu Glu Ile Glu Glu Ile
 1 1

att gag aat tca aat aat att att gag gag aag atc att att att att 318
 Lys Glu Arg Leu Arg Lys Arg Arg Glu Glu Lys Leu Leu Arg Asp Ala
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att att att att att att att att att att att att att att att att 319

0213: Homo sapiens

0220:

0221: CDS

0222: (754,...,4169)

0400: 25

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Met Arg Pro Phe Phe Leu Leu

1

5

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Cys Phe Ala Leu Pro Gly Leu Leu His Ala Gln Gln Ala Cys Ser Arg
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Gly Ala Cys Tyr Pro Pro Val Gly Asp Leu Leu Val Gly Arg Thr Arg
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Phe Leu Arg Ala Ser Ser Thr Cys Gly Leu Thr Lys Pro Glu Thr Tyr
40 45 50 55

tgc acc cag tat ggc gag tgg cag atg aaa tgc tgc aag tgt gac tcc 1020
Cys Thr Gln Tyr Gly Glu Trp Gln Met Lys Cys Cys Lys Cys Asp Ser
60 65 70

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Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala

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Ser Ser Gly Pro Met Arg Trp Trp Gln Ser Gln Asn Asp Val Asn Pro
80 85 90

ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 1200
Val Ser Leu Gln Ser Asp Leu Asp Ala Ala Ala Ala Ala Ala Ala

140

145

150

gac tgc acc tcc acc ttc cat cgg gtc cgc cag ggt cgg ttc cag ttc 1254
 Asp Cys Thr Ser Thr Phe Pro Arg Val Arg Gln Gly Arg Pro Gln Ser
 155 160 165

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 Trp Gln Asp Val Arg Cys Gln Ser Leu Pro Gln Arg Pro Asn Ala Arg
 170 175 180

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 185 190 195

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 Asn Leu Arg Val Asn Phe Thr Arg Leu Ala Pro Val Pro Gln Arg Gly
 220 225 230

tac cac cct ccc agc gcc tac tat gct gtg ttc cag ctc agt atg cag 1494
 Tyr His Pro Pro Ser Ala Tyr Tyr Ala Val Ser Gln Leu Arg Leu Gln
 235 240 245

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 Gly Ser Cys Phe Cys His Gly His Ala Asp Arg Cys Ala Pro Lys Pro
 250 255 260

ggg gcc tct gca ggc ccc tcc acc gct gtg cag atc cac gat gtc tgt 1590
 Gly Ala Ser Ala Gly Pro Ser Thr Ala Val Gln Val His Asp Val Cys
 265 270 275

gtc tgc cag cac aac act gcc ggc cca aat tgt gag cgc tgt gaa ccc 1638
 Val Cys Gln His Asn Thr Ala Gly Pro Asn Cys Glu Arg Cys Ala Pro
 280 285 290 295

tta tta aat aat tta cct tta aat tta tta tta tta tta tta tta tta 1686
 Phe Tyr Asn Asn Arg Pro Trp Arg Ile Ala Gln Gly Gln Asp Ala His
 300 305 310 315 320 325 330 335 340 345 350

tta tta aat aat tta cct tta aat tta tta tta tta tta tta tta tta 1734
 Glu Cys Gln Arg Cys Asp Cys Asn Gly His Ser Gln Thr Cys His Phe
 315 320 325 330 335 340 345 350

tta tta aat aat tta cct tta aat tta tta tta tta tta tta tta tta 1782
 Arg Ile Ala Val Phe Ala Ala Ser Gln Arg Arg Tyr Gly Arg Val Tyr
 355 360 365 370 375 380 385 390 395 400

tta tta aat aat tta cct tta aat tta tta tta tta tta tta tta tta 1830
 Glu Phe Arg Ile Ser Ile Ser Ile Ile Ile Ile Ile Ile Ile Ile
 405 410 415 420 425 430 435 440 445 450

tgc atc tcc tgc gag tgt gat ccg gat ggg gca gtg cca ggg gct ccc 1926
Cys Ile Ser Cys Glu Cys Asp Pro Asp Gly Ala Val Pro Gly Ala Pro
380 385 390

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Cys Asp Pro Val Thr Gly Gln Cys Val Cys Lys Glu His Val Gln Gly
395 400 405

gag cgc tgt gac cta tgc aag ccg ggc ttc act gga ctc acc tac gcc 2022
Glu Arg Cys Asp Leu Cys Lys Pro Gly Phe Thr Gly Leu Thr Tyr Ala
410 415 420

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Asn Pro Gln Gly Cys His Arg Cys Asp Cys Asn Ile Leu Gly Ser Arg
425 430 435

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Arg Asp Met Pro Cys Asp Glu Glu Ser Gly Arg Cys Leu Cys Leu Pro
440 445 450 455

aac gtg gtg ggt ccc aaa tgt gac cag tgt gct ccc tac cag tgg aag 2166
Asn Val Val Gly Pro Lys Cys Asp Gln Cys Ala Pro Tyr His Trp Lys
460 465 470

ctg gcc agt ggc cag ggc tgt gaa ccg tgt gcc tgc gac ccg cag aac 2214
Leu Ala Ser Gly Gln Gly Cys Glu Pro Cys Ala Cys Asp Pro His Asn
475 480 485

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Glu Gly Phe Gly Gly Leu Met Cys Ser Ala Ala Ala Ile Arg Gln Cys
505 510 515

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Pro Asp Arg Thr Tyr Gly Asp Val Ala Thr Gly Cys Arg Ala Cys Arg
520 525 530

tgc gac ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 2406
Tyr Arg Ile Arg Gly Thr Gln Gly Leu Gly Tyr Arg Lys Ala Ser Gly
540 545 550

cgc tgc ctc tgc cgc cct ggc ttg acc ggg ccc cgc tgt gac cag tgc 2454
Arg Cys Leu Cys Arg Pro Gly Leu Thr Gly Pro Arg Cys Asp Gln Cys
555 560 565

a!
mX

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 Gly Arg Leu Arg Asn Ala Thr Ala Ser Leu Trp Ser Gly Pro Gly Leu
 600 605 610 615

gag gac agt ggt atg gga taa ggg atc cta ggt gaa aag agt aag att 2646
 Glu Asp Arg Gly Leu Ala Ser Arg Ile Leu Asp Ala Lys Ser Lys Ile
 620 625 630

gag cag atc cga gaa gtt cta agt agc cca gaa gtc aca gag atg gag 2694
 Glu Gln Ile Arg Ala Val Leu Ser Ser Pro Ala Val Thr Glu Gln Gln
 635 640 645

atg gct cag gta gac agt ggc atc cta cca cta agt cga aat cta cag 2742
 Val Ala Gln Val Ala Ser Ala Ile Leu Ser Leu Arg Arg Thr Leu Gln
 650 655 660

gag atg cag atg gat atg ccc atg gag gag gag agt ttg tcc ctt cag 2790
 Gly Leu Gln Leu Asp Leu Pro Leu Glu Glu Glu Thr Leu Ser Leu Pro
 665 670 675

aga gac atg gag agt ctt gac aga agt ttc aat ggt cta ctt aat atg 2838
 Arg Asp Leu Glu Ser Leu Asp Arg Ser Phe Asn Gly Leu Leu Thr Met
 680 685 690 695

tat cag agg aag agg gag cag ttt gaa aaa ata agc agt gct gat cct 2886
 Tyr Gln Arg Lys Arg Glu Gln Phe Glu Lys Ile Ser Ser Ala Asp Pro
 700 705 710

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 715 720 725

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 Ala Ala Gln Gln Val Ser Asp Ser Ser Arg Leu Leu Asp Gln Leu Arg
 730 735 740

gac agc cgg aca gag gaa gag agt atg gtc cgg gag ggc gga gga gga 3030
 Asp Ser Arg Arg Glu Ala Gln Arg Leu Val Arg Glu Ala Gly Gly Gly
 745 750 755

tta tta tta tta tta tta tta tta tta tta tta tta tta tta tta tta 3078
 Lys Lys Thr Lys Ser Ile Lys Leu Val Ala Leu Arg Leu Ala Met Ser
 760 765 770

tgg ttg ctt gac atg aca cca aat ttc aac aat cta agt ggt ggt ggt 3126
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 775 780 785

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 790 795 800

Arg Ala Gly Gly Ala Phe Leu Met Ala Gly Gln Val Ala Glu Gln Leu
825 830 835

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Arg Gly Phe Asn Ala Gln Leu Gln Arg Thr Arg Gln Met Ile Arg Ala
840 845 850 855

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Ala Glu Glu Ser Ala Ser Gln Ile Gln Ser Ser Ala Gln Arg Leu Glu
860 865 870

acc cag gtg agc gcc agc cgc tcc cag atg gag gaa gat gtc aga cgc 3414
Thr Gln Val Ser Ala Ser Arg Ser Gln Met Glu Glu Asp Val Arg Arg
875 880 885

aca cgg ctc cta atc caa cag gtc cgg gac ttc cta aca gac ccc gac 3462
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905 910 915

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Trp Leu Pro Thr Asp Ser Ala Thr Val Leu Gln Lys Met Asn Glu Ile
920 925 930 935

cag gcc att gca gcc agg ctc ccc aac gtg gac ttg gtg ctg tcc cag 3606
Gln Ala Ile Ala Ala Arg Leu Pro Asn Val Asp Leu Val Leu Ser Gln
940 945 950

acc aag cag gac att gcg cgt gcc cgc cgg ttg cag gct gag gct gag 3654
Thr Lys Gln Asp Ile Ala Arg Ala Arg Arg Leu Gln Ala Glu Ala Glu
955 960 965

gaa gcc agg agc cga gcc cat gca gtg gag gcc cag gtg gaa gat gtg 3702
Glu Ala Arg Ser Arg Ala His Ala Val Glu Gly Gln Val Glu Asp Val
970 975 980

atg ggt aac tta ttt ctt ttt aca tgg tta ttg ctt ttt ttt ttt 3750
Val Gly Asn Leu Arg Gln Gly Thr Val Ala Leu Val Val Ala Val Arg
985 990 995

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1000 1005 1010 1015

atg ggt tta tta tta tta tta tta tta tta tta tta tta tta tta 3846
Val Gly Asn Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
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1050

1055

1060

gaa gaa ggt ttt aac aac aac gaa ttg agt gcc aac gag gga ttt gag 4340
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 1065 1070 1075

aga ala aac aac aac ttt ggt gag ttg aag gac cgg ttt ggt aac agt 4350
 Arg Ile Lys Gln Lys Tyr Ala Glu Leu Lys Asp Arg Leu Gly Gln Ser
 1080 1085 1090 1095

tac atg ctg ggt gag gag ggt gcc cgg atc cag agt gtg aag aca gag 4360
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 1100 1105 1110

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 1115 1120 1125

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 1130 1135 1140

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 Ser Ala Asp Leu Thr Gly Leu Glu Lys Arg Val Glu Gln Ile Arg Asp
 1145 1150 1155

cac atc aat ggg cgc gtg ctg tac tat gcc acc tgc aag tgatgctaca 4400
 His Ile Asn Gly Arg Val Leu Tyr Tyr Ala Thr Cys Lys
 1160 1165 1170

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4490
 4500
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 4530

4540
 4550
 4560 (134)... (508)

4570
 4580

4590
 4600

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ctt aat gga gtc aag ctg gtc gtc gag aca ccc gag aag aac ctg ttc 467
 Leu Asn Gly Val Lys Leu Val Val Ala Thr Ile Glu Glu Thr Leu Ile
 45 50 55

ctt aat gga gtc aag ctg gtc gtc gag aca ccc gag aag aac ctg ttc 468
 Thr Arg Ile Leu Thr Val Gly Pro Gln Ser Leu Gly Ser Glu Ala Leu
 60 65 70 75

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 Ala Ser Pro Thr Arg Arg Ala Ala Cys Thr Val Phe Thr Ala Thr Ala
 80 85 90 95

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 Ser Thr Arg Thr Trp Gly Pro Pro Leu Pro His Ser Leu Thr Gly Cys
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 110 115 120

ent

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 Met Glu Leu Ile Ile Val Ser Ala Ile Leu Leu Ile Val

30	35	40	45	
aga ggt tat ggt gat aaa ctc atc tgg act aag aaa tat gaa gaa gct	318			
Arg Gly Trp Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Gln Glu Ala				
65	70	75	80	
cta tat aag tct aag aca age aac aaa ctt ttg att att att cat cac	324			
Leu Tyr Lys Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His				
65	70	75		
ttg gat gag tgc cca cac agt caa gct tta aag aaa gtg ttt gct gaa	351			
Leu Asp Glu Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu				
80	85	90		
aat aaa gaa atc aag aaa ttg gca gag aag ttt gtc ctc ctc aat ctg	399			
Asn Lys Glu Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu				
95	100	105		
gtt tat gaa aca act gac aaa cac ctt tct cct gat ggc aag tat gtc	447			
Val Tyr Glu Thr Thr Asp Lys His Leu Ser Pro Asp Gly Gln Tyr Val				
110	115	120	125	
ccc agg att atg ttt gtt gac cca tct ctg aca gtt aga gcc gat atc	495			
Pro Arg Ile Met Phe Val Asp Pro Ser Leu Thr Val Arg Ala Asp Ile				
130	135	140		
act gga aga tat tca aac cgt ctc tat gct tac gaa cct gca gat aca	543			
Thr Gly Arg Tyr Ser Asn Arg Leu Tyr Ala Tyr Glu Pro Ala Asp Thr				
145	150	155		
gct ctg ttg ctt gac aac atg aag aaa gct ctc aag ttg ctg aag act	591			
Ala Leu Leu Leu Asp Asn Met Lys Lys Ala Leu Lys Leu Leu Lys Thr				
160	165	170		
gaa ttg taagaaataaatatataaa gcaatctctgt ctgtcaggtt ttgagacttg	647			
Glu Leu				
175				

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